WHAT IS CLAIMED IS:

1. A method for identifying and/or quantifying a biological organism or component thereof comprising:

contacting a target comprising the organism or components thereof with capture molecules bound to an insoluble solid support; and

detecting, quantifying and/or recording a signal resulting from the specific binding between said targets and their corresponding specific capture molecules,

wherein said capture molecules are bound to an insoluble solid support surface at a specific location in an array, said array having a density of at least 4 different bound capture molecules/cm^2 of solid support surface, and

wherein the binding between targets and their corresponding capture molecules forms said signal at the expected location and the detection of said single signal allows discrimination of a target being specific for said organism or its components from other related organisms or other related components.

2. The method of claim 1, wherein said organism or component is present in a sample among at least 2 other related organisms or components.

3. The method of claim 1, wehrein said organism or component is present in a sample among at least 4 other related organisms or components.

4. The method of claim 1, further comprising extracting orginal components from said organism.

5. The method of claim 1, further comprising labeling said organism or its components as targets.

6. The method of claim 1, wherein said organism is a microorganism.

7. The method of claim 1, further comprising the step of identifying and/or quantifying the presence of several groups, sub-groups or sub-sub-groups of components or organisms comprising said components being related to each other until possible individual components or organisms wherein the binding between targets and corresponding specific capture molecules forms a signal at an expected location allowing the identification of a target specific of a group, sub-group or sub-sub-group of components or organisms comprising said components.

8. The method of claim 7, wherein the array contains two categories of capture molecules, a first one being specific for individual target components or their sub-groups and the second one being specific for all the components of the group.

9. The method of claim 1, wherein the components to detect are nucleotide sequences amplified or copied as targets to be hybridized on specific capture nucleotide sequences bound to the solid support surface as arrays.

10. The method of claim 9, wherein the first category of capture molecules has a sequence length specific of the target of about 3 and about 60 bases and wherein the second category of capture nucleotide sequences has a sequence length specific of the target comprised between about 10 and about 1000 bases.

11. The method of claim 10, wherein said second category of capture nucleotide sequences has a sequence length specific of the target comprised between about 100 and 600 bases.

12. The method of claim 9, wherein the amplified target sequences are homologous polynucleotides and are discriminated on the array upon corresponding polynucleotide capture sequences.

13. The method of claim 9, wherein the amplified original polynucleotide sequences are DNA nucleotide sequences.

14. The identification method of claim 9, wherein all or most of the amplified sequences are obtained by PCR with the same primer pair.

15. The method of claim 9, wherein the presence of any amplified sequence is firstly detected during the genetic amplification cycles and thereafter identified on the array.

16. The method of claim 9, wherein the step of detecting the presence of any amplified sequences and the genetic amplification step are performed in a same chamber.

17. The method of claim 9, wherein the amplified nucleotide sequence is mRNA first retrotranscribed into cDNA with the same primer pair.

18. The method of claim 9, wherein the nucleotide sequences are copied by using the same primer pair.

19. The method of claim 9, wherein the specific sequence of the capture nucleotide sequence, able to hybridize with their corresponding target nucleotide sequence, is separated from the surface of the solid support by a spacer having at least 6.8 nm.

20. The method of claim 19, wherein said spacer is a nucleotide sequence of between about 15 and about 1000 bases.

21. The method of claim 19, wherein said spacer is a nucleotide sequence of between about 30 and about 120 bases.

22. The method of claim 19, wherein the spacer is a polymeric chain of at least 10 atoms, selected from the group consisting of poly-ethyleneglycol, polyaminoacids, polyacrylamides, poly-aminosaccharides, polyglucides, polyamides, polyacrylates, polycarbonates, polyepoxides, poly-ester and a mixture thereof.

23. The method of claim 19, wherein said polymeric chain is branched.

24. The method of claim 9, wherein the length of the specific sequence of the capture nucleotide sequence able to hybridize with the corresponding target nucleotide sequences is comprised between about 5 and about 60 bases.

25. The method of Claim 24, wherein the corresponding target nucleotide sequences is comprised between about 20 and about 30 bases.

26. The method of claim 9, wherein the density of the capture nucleotide sequences bound to the solid support surface at a specific location is greater than 10 fmoles per cm^2 of solid support surface.

27. The method of claim 9, wherein the density of the capture nucleotide sequences bound to the solid support surface at a specific location is greater than 100 fmoles per cm^2 of solid support surface.

28. The method of claim 9, wherein the capture nucleotide sequences bound to the solid support surface at a specific location are bound to the support by covalent binding.

29. The method of claim 9, wherein the capture nucleotide sequences bound to the solid support surface at a specific location are polynucleotides.

30. The method of claim 9, wherein the target nucleotide sequence(s) to be detected present(s) a homology of greater than about 40% with other homologous nucleotide sequences.

31. The method of claim 9, wherein the target nucleotide sequence(s) to be detected present(s) a homology of greater than about 60% with other homologous nucleotide sequences.

32. The method of claim 9, wherein the target nucleotide sequence(s) to be detected present(s) a homology of greater than about 80% with other homologous nucleotide sequences.

33. The method of claim 9, wherein the target nucleotide sequences are labelled by a marker and wherein the signal resulting from hybridization by complementary bases pairing between the target nucleotide sequence and its corresponding capture nucleotide sequence is obtained from the detection of said marker.

34. The method of claim 9, wherein the target nucleotide sequences are cut into pieces before putting into contact with the single stranded capture nucleotide sequences bound to the solid support.

35. The method of claim 9, wherein other primers are present in the amplification step for the amplification of other nucleotide sequences, such as an antibiotic resistance determining sequence.

36. The method of claim 9, wherein the nucleotide sequences to be detected and/or be quantified are RNA sequences submitted to a retro-transcription of the 3' or 5' end by using a member selected from the group consisting of a consensus primer and a stopper sequence.

37. The method of claim 9, wherein the solid support surface comprises capture nucleotide sequences specific for the binding of homologous target nucleotide sequences together with a consensus sequence for a common detection.

38. The method of claim 9, wherein the solid support comprises capture nucleotide sequences specific for the identification of two or more staphylococcus species together with a consensus sequence for a *Staphylococcus* genus identification.

39. The method of claim 9, wherein the original sequence to be identified and/or quantified in the sample differs from at least one of its homologous sequences present in the sample by one or more base(s).

40. The method of claim 9, wherein the arrays contained two to four capture nucleotide sequences differing from each other by one or more base(s).

41. The method of claim 1, wherein the component to be detected and/or quantified is a protein and the capture molecule an antibody or an hypervariable portion thereof.

42. The method of claim 41, wherein the target is bound to the capture molecule by one of its epitopes.

43. The method of claim 37, wherein the capture molecule is a monoclonal antibody or an hypervariable portion thereof.

44. The method of claim 1, wherein the quantification of the organism present in the biological sample is obtained by the quantification of the signal.

45. The method of claim 1, wherein the insoluble solid support is selected from the group consisting of glass, an electronic device, a silicon support, a plastic support, silica, metal and a mixture thereof, wherein said support is prepared in a prepared in a format selected from the group consisting of slides, discs, gel layers and microbeads.

46. The method of claim 1, wherein the microorganism to be identified and/or quantified in the sample belongs to the Staphylococci species selected from the group consisting of *S. aureus, S. epidermidis, S. saprophyticus, S. hominis* and *S. haemolyticus*.

47. The method of claim 1, wherein the microorganism to be identified and/or quantified in the sample belong to the Mycobacteria genus.

48. The method of claim 1, wherein the component to be identified and/or quantified in the sample is a sequence which belongs to the MAGE family.

49. The method of claim 1, wherein the component to be identified and/or quantified in the sample is a sequence which belongs to the *HLA-A* family.

50. The method of claim 1, wherein the component to be identified and/or quantified in the sample is a G coupled receptor.

51. The method of claim 49, wherein the component to be identified and/or quantified in the sample is a dopamine receptor.

52. The method of claim 47, wherein the component to be identified and/or quantified in the sample is a choline receptor.

53. The method of claim 47, wherein the component to be identified and/or quantified in the sample is a histamine receptor.

54. The method of claim 1, wherein the component to be identified and/or quantified in the sample is a sequence which belongs the cytochrome P450 forms family.

55. The method of claim1, wherein the microorganism to be identified and/or quantified in the sample belongs to the Gram-positive or Gram-negative family bacteria.

56. The method of claim 7, wherein the group, sub-group or individual targets correspond to families, genus, species, subtypes or individual organisms.

57. The method of claim 7, wherein the families, genus, species, subtypes or individuals are bacteria.

58. The method of claim 57, wherein bacteria belonging to at least two of the genus families selected from the group consisting of Staphylococcus, Enterococcus, Streptococcus, Haemolyticus, Pseudomonas, Campylobacter, Enterobacter, Neisseria, Proteus, Salmonella, Simonsiella, Riemerella, Escherichia, Neisseria, Meningococcus, Moraxella, Kingella, Chromobacterium and Branhamella.

59. The method of claim 9, wherein the identification of the nucleotide sequences allows an identification of the polymorphism of an organism.

60. The method of claim 9, wherein the identification of the nucleotide sequences allows the genotyping of an organism.

61. The method of claim 9, wherein the identification of the nucleotide sequences allows the identification of a single nucleotide polymorphism.

62. A diagnostic and/or quantification kit which comprises means and media for performing the method of claim 1, including an insoluble solid support surface upon which capture molecules are bound, said capture molecules being disposed upon the surface of the solid support according to an array with a density of at least 4 single stranded capture nucleotide sequences/cm^2 of solid support surface.

63. The diagnostic and/or quantification kit of claim 62, wherein the capture molecules are single stranded capture nucleotide sequences containing a sequence of a length comprised between about 3 and about 60 bases, and being specific for a target nucleotide sequence to be identified and/or quantified and wherein the target nucleotide sequences and their corresponding capture sequences have a total length comprised between about 30 and about 1000 bases.

64. The diagnostic kit of claim 62, wherein all capture molecules are polynucleotides.

65. The diagnostic kit of claim 62, wherein the insoluble solid support is selected from the group consisting of glass, an electronic device, a silicon support, a plastic support,

silica, metal and a mixture thereof, wherein said support is prepared in a prepared in a format selected from the group consisting of slides, discs, gel layers and microbeads.

66. The diagnostic kit of claim 62, wherein the capture molecules are specific to a target component to be detected and/or quantified, said component being specific for a gene or protein selected from the group consisting of *Staphylococcus* species, MAGE family, HLA family, G coupled receptor family, cytochrome P450 forms family and genetically modified plants family.

67. The diagnostic kit of claim 62, for the identification and/or quantification of 3 or more SNP sequences.

68. The diagnostic kit of claim 62, for the identification of the polymorphism of an organism.

69. The diagnostic kit of claim 62, comprising biochips, for the identification of the genotyping of an organism.

70. The diagnostic kit of claim 62, comprising chambers for performing a genetic amplification together with the identification and/or quantification of amplified nucleotide sequences.

71. The diagnostic kit of claim 62, comprising chambers wherein the detection for the presence of any amplified sequences of an organism and the genetic amplification are performed in the same chamber.

72. The diagnostic kit of claim 68, wherein said organism is a microorganism.

73. The diagnostic kit of claim 69, wherein said organism is a microorganism.

74. The diagnostic kit of claim 71, wherein said organism is a microorganism.

75. A diagnostic and/or quantification apparatus for detecting or quantifying an organism or component possibly present in a sample containing other related organisms which comprises:

capture molecules bound to an insoluble solid support surface at specific locations according to an array, said capture molecules being able to discriminate between related organisms or components, said array having a density of at least 4 bound capture molecules in a discrete region per cm^2 solid support surface;

a detection and/or quantification device of a signal formed at the location of the binding between said target molecule obtained or corresponding to said organism or component and said capture molecule; and

a computer program for recognizing the discrete regions bearing the bound target molecules upon its corresponding capture molecules and their locations.

76. The apparatus of Claim 75 further comprising components for correlating the presence of the signal at these locations with the diagnostic and/or the quantification of the said organism or component.

77. The diagnostic and/or quantification apparatus of claim 75, further comprising a reading device of information recorded upon a surface of said solid support.

78. The diagnostic and/or quantification apparatus of claim 75, further comprising genetic amplification components for the amplification of target nucleotide sequences obtained from said organism or a component thereof by PCR performed previously or in real time together with the identification of an organism or its components.

79. The diagnostic and/or quantification apparatus of claim 75, wherein said organism is a microorganism.

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